

Jens B Nielsen

List of Publications by Year in descending order

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895
papers

85,682
citations

527

127
h-index

930

240
g-index

1010
all docs

1010
docs citations

1010
times ranked

79571
citing authors

#	ARTICLE	IF	CITATIONS
1	Tissue-based map of the human proteome. <i>Science</i> , 2015, 347, 1260419.	6.0	10,802
2	Analysis of the Human Tissue-specific Expression by Genome-wide Integration of Transcriptomics and Antibody-based Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 397-406.	2.5	2,819
3	Gut metagenome in European women with normal, impaired and diabetic glucose control. <i>Nature</i> , 2013, 498, 99-103.	13.7	2,401
4	Genome sequencing and analysis of the versatile cell factory <i>Aspergillus niger</i> CBS 513.88. <i>Nature Biotechnology</i> , 2007, 25, 221-231.	9.4	1,047
5	Symptomatic atherosclerosis is associated with an altered gut metagenome. <i>Nature Communications</i> , 2012, 3, 1245.	5.8	970
6	Engineering Cellular Metabolism. <i>Cell</i> , 2016, 164, 1185-1197.	13.5	953
7	Genome-Scale Reconstruction of the <i>Saccharomyces cerevisiae</i> Metabolic Network. <i>Genome Research</i> , 2003, 13, 244-253.	2.4	931
8	A community-driven global reconstruction of human metabolism. <i>Nature Biotechnology</i> , 2013, 31, 419-425.	9.4	920
9	Fuel ethanol production from lignocellulose: a challenge for metabolic engineering and process integration. <i>Applied Microbiology and Biotechnology</i> , 2001, 56, 17-34.	1.7	788
10	Minimum Information about a Biosynthetic Gene cluster. <i>Nature Chemical Biology</i> , 2015, 11, 625-631.	3.9	715
11	Enriching the gene set analysis of genome-wide data by incorporating directionality of gene expression and combining statistical hypotheses and methods. <i>Nucleic Acids Research</i> , 2013, 41, 4378-4391.	6.5	684
12	Roux-en-Y Gastric Bypass and Vertical Banded Gastroplasty Induce Long-Term Changes on the Human Gut Microbiome Contributing to Fat Mass Regulation. <i>Cell Metabolism</i> , 2015, 22, 228-238.	7.2	638
13	Voluntary Running Suppresses Tumor Growth through Epinephrine- and IL-6-Dependent NK Cell Mobilization and Redistribution. <i>Cell Metabolism</i> , 2016, 23, 554-562.	7.2	572
14	Uncovering transcriptional regulation of metabolism by using metabolic network topology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2685-2689.	3.3	553
15	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. <i>Nature Biotechnology</i> , 2008, 26, 1155-1160.	9.4	530
16	Recon3D enables a three-dimensional view of gene variation in human metabolism. <i>Nature Biotechnology</i> , 2018, 36, 272-281.	9.4	520
17	Mass spectrometry in metabolome analysis. <i>Mass Spectrometry Reviews</i> , 2005, 24, 613-646.	2.8	513
18	An interlaboratory comparison of physiological and genetic properties of four <i>Saccharomyces cerevisiae</i> strains. <i>Enzyme and Microbial Technology</i> , 2000, 26, 706-714.	1.6	488

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19	Genome-scale metabolic modelling of hepatocytes reveals serine deficiency in patients with non-alcoholic fatty liver disease. <i>Nature Communications</i> , 2014, 5, 3083.	5.8	461
20	Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. <i>Nature Methods</i> , 2021, 18, 747-756.	9.0	403
21	Assessing the Human Gut Microbiota in Metabolic Diseases. <i>Diabetes</i> , 2013, 62, 3341-3349.	0.3	384
22	Reconstruction of Genome-Scale Active Metabolic Networks for 69 Human Cell Types and 16 Cancer Types Using INIT. <i>PLoS Computational Biology</i> , 2012, 8, e1002518.	1.5	381
23	Evolutionary programming as a platform for in silico metabolic engineering. <i>BMC Bioinformatics</i> , 2005, 6, 308.	1.2	374
24	Metabolic Engineering of <i>Saccharomyces cerevisiae</i> . <i>Microbiology and Molecular Biology Reviews</i> , 2000, 64, 34-50.	2.9	369
25	Altered sterol composition renders yeast thermotolerant. <i>Science</i> , 2014, 346, 75-78.	6.0	368
26	Metabolic engineering of <i>Saccharomyces cerevisiae</i> : a key cell factory platform for future biorefineries. <i>Cellular and Molecular Life Sciences</i> , 2012, 69, 2671-2690.	2.4	367
27	Improving the phenotype predictions of a yeast genome-scale metabolic model by incorporating enzymatic constraints. <i>Molecular Systems Biology</i> , 2017, 13, 935.	3.2	367
28	Global metabolite analysis of yeast: evaluation of sample preparation methods. <i>Yeast</i> , 2005, 22, 1155-1169.	0.8	365
29	The RAVEN Toolbox and Its Use for Generating a Genome-scale Metabolic Model for <i>Penicillium chrysogenum</i> . <i>PLoS Computational Biology</i> , 2013, 9, e1002980.	1.5	364
30	Flux Distributions in Anaerobic, Glucose-Limited Continuous Cultures of <i>Saccharomyces Cerevisiae</i> . <i>Microbiology (United Kingdom)</i> , 1997, 143, 203-218.	0.7	358
31	<i>Saccharomyces cerevisiae</i> phenotypes can be predicted by using constraint-based analysis of a genome-scale reconstructed metabolic network. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 13134-13139.	3.3	345
32	Quantifying Diet-Induced Metabolic Changes of the Human Gut Microbiome. <i>Cell Metabolism</i> , 2015, 22, 320-331.	7.2	345
33	Network Identification and Flux Quantification in the Central Metabolism of <i>Saccharomyces cerevisiae</i> under Different Conditions of Glucose Repression. <i>Journal of Bacteriology</i> , 2001, 183, 1441-1451.	1.0	334
34	Identification of anticancer drugs for hepatocellular carcinoma through personalized genome-scale metabolic modeling. <i>Molecular Systems Biology</i> , 2014, 10, 721.	3.2	331
35	Comparative genomics of citric-acid-producing <i>Aspergillus niger</i> ATCC 1015 versus enzyme-producing CBS 513.88. <i>Genome Research</i> , 2011, 21, 885-897.	2.4	329
36	OptFlux: an open-source software platform for in silico metabolic engineering. <i>BMC Systems Biology</i> , 2010, 4, 45.	3.0	321

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37	Analysis of gut microbial regulation of host gene expression along the length of the gut and regulation of gut microbial ecology through MyD88. <i>Gut</i> , 2012, 61, 1124-1131.	6.1	321
38	An Integrated Understanding of the Rapid Metabolic Benefits of a Carbohydrate-Restricted Diet on Hepatic Steatosis in Humans. <i>Cell Metabolism</i> , 2018, 27, 559-571.e5.	7.2	321
39	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	9.4	314
40	In silico aided metabolic engineering of <i>Saccharomyces cerevisiae</i> for improved bioethanol production. <i>Metabolic Engineering</i> , 2006, 8, 102-111.	3.6	311
41	Production of fatty acid-derived oleochemicals and biofuels by synthetic yeast cell factories. <i>Nature Communications</i> , 2016, 7, 11709.	5.8	306
42	Increasing NADH oxidation reduces overflow metabolism in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 2402-2407.	3.3	302
43	The gut microbiota modulates host amino acid and glutathione metabolism in mice. <i>Molecular Systems Biology</i> , 2015, 11, 834.	3.2	291
44	Metabolic engineering. <i>Applied Microbiology and Biotechnology</i> , 2001, 55, 263-283.	1.7	285
45	A comprehensive comparison of RNA-Seq-based transcriptome analysis from reads to differential gene expression and cross-comparison with microarrays: a case study in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2012, 40, 10084-10097.	6.5	285
46	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. <i>Nature</i> , 2020, 581, 310-315.	13.7	283
47	Modeling isotopomer distributions in biochemical networks using isotopomer mapping matrices. , 1997, 55, 831-840.		282
48	Characterization of different promoters for designing a new expression vector in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2010, 27, 955-964.	0.8	281
49	Establishing a platform cell factory through engineering of yeast acetyl-CoA metabolism. <i>Metabolic Engineering</i> , 2013, 15, 48-54.	3.6	268
50	Metabolic engineering of yeast for production of fuels and chemicals. <i>Current Opinion in Biotechnology</i> , 2013, 24, 398-404.	3.3	263
51	The human secretome. <i>Science Signaling</i> , 2019, 12, .	1.6	259
52	Lipid engineering combined with systematic metabolic engineering of <i>Saccharomyces cerevisiae</i> for high-yield production of lycopene. <i>Metabolic Engineering</i> , 2019, 52, 134-142.	3.6	251
53	Third-generation biorefineries as the means to produce fuels and chemicals from CO ₂ . <i>Nature Catalysis</i> , 2020, 3, 274-288.	16.1	245
54	De novo production of resveratrol from glucose or ethanol by engineered <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2015, 32, 1-11.	3.6	242

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55	De novo sequencing, assembly and analysis of the genome of the laboratory strain <i>Saccharomyces cerevisiae</i> CEN.PK113-7D, a model for modern industrial biotechnology. <i>Microbial Cell Factories</i> , 2012, 11, 36.	1.9	238
56	Kinetic models in industrial biotechnology – Improving cell factory performance. <i>Metabolic Engineering</i> , 2014, 24, 38-60.	3.6	238
57	Microbial acetyl-CoA metabolism and metabolic engineering. <i>Metabolic Engineering</i> , 2015, 28, 28-42.	3.6	237
58	EasyClone: method for iterative chromosomal integration of multiple genes <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2014, 14, 238-248.	1.1	236
59	The Metabolic Response of Heterotrophic <i>Arabidopsis</i> Cells to Oxidative Stress. <i>Plant Physiology</i> , 2007, 143, 312-325.	2.3	234
60	Characterization of chromosomal integration sites for heterologous gene expression in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2009, 26, 545-551.	0.8	233
61	Modeling <i>Lactococcus lactis</i> using a genome-scale flux model. <i>BMC Microbiology</i> , 2005, 5, 39.	1.3	231
62	RAVEN 2.0: A versatile toolbox for metabolic network reconstruction and a case study on <i>Streptomyces coelicolor</i> . <i>PLoS Computational Biology</i> , 2018, 14, e1006541.	1.5	228
63	Understanding the interactions between bacteria in the human gut through metabolic modeling. <i>Scientific Reports</i> , 2013, 3, 2532.	1.6	224
64	An atlas of human metabolism. <i>Science Signaling</i> , 2020, 13, .	1.6	223
65	It Is All about MetabolicFluxes. <i>Journal of Bacteriology</i> , 2003, 185, 7031-7035.	1.0	221
66	Advances in metabolic engineering of yeast <i>Saccharomyces cerevisiae</i> for production of chemicals. <i>Biotechnology Journal</i> , 2014, 9, 609-620.	1.8	221
67	Glucose repression in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2015, 15, fov068.	1.1	220
68	Isotopomer Analysis Using GC-MS. <i>Metabolic Engineering</i> , 1999, 1, 282-290.	3.6	218
69	Integration of clinical data with a genome-scale metabolic model of the human adipocyte. <i>Molecular Systems Biology</i> , 2013, 9, 649.	3.2	217
70	A consensus <i>S. cerevisiae</i> metabolic model Yeast8 and its ecosystem for comprehensively probing cellular metabolism. <i>Nature Communications</i> , 2019, 10, 3586.	5.8	217
71	Production of plant sesquiterpenes in <i>Saccharomyces cerevisiae</i> : Effect of <i>ERG9</i> repression on sesquiterpene biosynthesis. <i>Biotechnology and Bioengineering</i> , 2008, 99, 666-677.	1.7	216
72	Genome-scale analysis of <i>Streptomyces coelicolor</i> A3(2) metabolism. <i>Genome Research</i> , 2005, 15, 820-829.	2.4	215

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73	Dynamic control of gene expression in <i>Saccharomyces cerevisiae</i> engineered for the production of plant sesquiterpene β -santalene in a fed-batch mode. <i>Metabolic Engineering</i> , 2012, 14, 91-103.	3.6	215
74	Reprogramming Yeast Metabolism from Alcoholic Fermentation to Lipogenesis. <i>Cell</i> , 2018, 174, 1549-1558.e14.	13.5	215
75	The Essence of Metabolic Engineering. , 1998, , 1-20.		214
76	Establishment of a yeast platform strain for production of p-coumaric acid through metabolic engineering of aromatic amino acid biosynthesis. <i>Metabolic Engineering</i> , 2015, 31, 181-188.	3.6	213
77	Reproducibility of Oligonucleotide Microarray Transcriptome Analyses. <i>Journal of Biological Chemistry</i> , 2002, 277, 37001-37008.	1.6	208
78	Growth-rate regulated genes have profound impact on interpretation of transcriptome profiling in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology</i> , 2006, 7, R107.	13.9	205
79	The next wave in metabolome analysis. <i>Trends in Biotechnology</i> , 2005, 23, 544-546.	4.9	204
80	Optimization of Ethanol Production in <i>Saccharomyces cerevisiae</i> by Metabolic Engineering of the Ammonium Assimilation. <i>Metabolic Engineering</i> , 2000, 2, 69-77.	3.6	200
81	Enhancing sesquiterpene production in <i>Saccharomyces cerevisiae</i> through in silico driven metabolic engineering. <i>Metabolic Engineering</i> , 2009, 11, 328-334.	3.6	199
82	Production of biopharmaceutical proteins by yeast. <i>Bioengineered</i> , 2013, 4, 207-211.	1.4	199
83	Integration of gene expression data into genome-scale metabolic models. <i>Metabolic Engineering</i> , 2004, 6, 285-293.	3.6	198
84	Global analysis of biosynthetic gene clusters reveals vast potential of secondary metabolite production in <i>Penicillium</i> species. <i>Nature Microbiology</i> , 2017, 2, 17044.	5.9	198
85	High-throughput screening for industrial enzyme production hosts by droplet microfluidics. <i>Lab on A Chip</i> , 2014, 14, 806-813.	3.1	195
86	Impact of synthetic biology and metabolic engineering on industrial production of fine chemicals. <i>Biotechnology Advances</i> , 2015, 33, 1395-1402.	6.0	195
87	Diversion of Flux toward Sesquiterpene Production in <i>Saccharomyces cerevisiae</i> by Fusion of Host and Heterologous Enzymes. <i>Applied and Environmental Microbiology</i> , 2011, 77, 1033-1040.	1.4	194
88	Improving Production of Malonyl Coenzyme A-Derived Metabolites by Abolishing Snf1-Dependent Regulation of Acc1. <i>MBio</i> , 2014, 5, e01130-14.	1.8	194
89	Metabolic model integration of the bibliome, genome, metabolome and reactome of <i>Aspergillus niger</i> . <i>Molecular Systems Biology</i> , 2008, 4, 178.	3.2	190
90	Establishing a synthetic pathway for high-level production of 3-hydroxypropionic acid in <i>Saccharomyces cerevisiae</i> via β -alanine. <i>Metabolic Engineering</i> , 2015, 27, 57-64.	3.6	185

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91	Glucose control in <i>Saccharomyces cerevisiae</i> : the role of MIG1 in metabolic functions. <i>Microbiology (United Kingdom)</i> , 1998, 144, 13-24.	0.7	181
92	Absolute Quantification of Protein and mRNA Abundances Demonstrate Variability in Gene-Specific Translation Efficiency in Yeast. <i>Cell Systems</i> , 2017, 4, 495-504.e5.	2.9	178
93	Simultaneous analysis of amino and nonamino organic acids as methyl chloroformate derivatives using gas chromatography–mass spectrometry. <i>Analytical Biochemistry</i> , 2003, 322, 134-138.	1.1	177
94	Rewiring carbon metabolism in yeast for high level production of aromatic chemicals. <i>Nature Communications</i> , 2019, 10, 4976.	5.8	177
95	Modelling of microbial kinetics. <i>Chemical Engineering Science</i> , 1992, 47, 4225-4270.	1.9	174
96	Advanced biofuel production by the yeast <i>Saccharomyces cerevisiae</i> . <i>Current Opinion in Chemical Biology</i> , 2013, 17, 480-488.	2.8	173
97	Systems Biology of Metabolism. <i>Annual Review of Biochemistry</i> , 2017, 86, 245-275.	5.0	173
98	Metabolite profiling of fungi and yeast: from phenotype to metabolome by MS and informatics. <i>Journal of Experimental Botany</i> , 2005, 56, 273-286.	2.4	172
99	Metabolic flux distributions in <i>Penicillium chrysogenum</i> during fed-batch cultivations. <i>Biotechnology and Bioengineering</i> , 1995, 46, 117-131.	1.7	170
100	Production of natural products through metabolic engineering of <i>Saccharomyces cerevisiae</i> . <i>Current Opinion in Biotechnology</i> , 2015, 35, 7-15.	3.3	170
101	Increasing galactose consumption by <i>Saccharomyces cerevisiae</i> through metabolic engineering of the GAL gene regulatory network. <i>Nature Biotechnology</i> , 2000, 18, 1283-1286.	9.4	168
102	Bioreaction Engineering Principles. , 2011, , .		168
103	Mathematical modelling of metabolism. <i>Current Opinion in Biotechnology</i> , 2000, 11, 180-186.	3.3	165
104	Sampling the Solution Space in Genome-Scale Metabolic Networks Reveals Transcriptional Regulation in Key Enzymes. <i>PLoS Computational Biology</i> , 2010, 6, e1000859.	1.5	164
105	A gRNA-tRNA array for CRISPR-Cas9 based rapid multiplexed genome editing in <i>Saccharomyces cerevisiae</i> . <i>Nature Communications</i> , 2019, 10, 1053.	5.8	164
106	Mapping the interaction of Snf1 with TORC1 in <i>Saccharomyces cerevisiae</i> . <i>Molecular Systems Biology</i> , 2011, 7, 545.	3.2	163
107	In silico genome-scale reconstruction and validation of the <i>Corynebacterium glutamicum</i> metabolic network. <i>Biotechnology and Bioengineering</i> , 2009, 102, 583-597.	1.7	162
108	Yeast Systems Biology: Model Organism and Cell Factory. <i>Biotechnology Journal</i> , 2019, 14, e1800421.	1.8	159

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109	Metabolic engineering of recombinant protein secretion by <i>Saccharomyces cerevisiae</i> . FEMS Yeast Research, 2012, 12, 491-510.	1.1	157
110	Harnessing Yeast Peroxisomes for Biosynthesis of Fatty-Acid-Derived Biofuels and Chemicals with Relieved Side-Pathway Competition. Journal of the American Chemical Society, 2016, 138, 15368-15377.	6.6	157
111	Quantitative analysis of metabolic fluxes in <i>Escherichia coli</i> , using two-dimensional NMR spectroscopy and complete isotopomer models. Journal of Biotechnology, 1999, 71, 175-189.	1.9	154
112	Linking high-resolution metabolic flux phenotypes and transcriptional regulation in yeast modulated by the global regulator Gcn4p. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 6477-6482.	3.3	154
113	A trispecies <i>Aspergillus</i> microarray: Comparative transcriptomics of three <i>Aspergillus</i> species. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 4387-4392.	3.3	152
114	Metabolic engineering strategies for microbial synthesis of oleochemicals. Metabolic Engineering, 2015, 29, 1-11.	3.6	152
115	Systems biology of antibiotic production by microorganisms. Natural Product Reports, 2007, 24, 1262.	5.2	151
116	Use of genome-scale microbial models for metabolic engineering. Current Opinion in Biotechnology, 2004, 15, 64-69.	3.3	150
117	Human gut microbiota and healthy aging: Recent developments and future prospective. Nutrition and Healthy Aging, 2016, 4, 3-16.	0.5	150
118	Metabolic network-based stratification of hepatocellular carcinoma reveals three distinct tumor subtypes. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11874-E11883.	3.3	149
119	High-throughput metabolic state analysis: the missing link in integrated functional genomics of yeasts. Biochemical Journal, 2005, 388, 669-677.	1.7	147
120	Measuring enzyme activities under standardized <i>in vivo</i> like conditions for systems biology. FEBS Journal, 2010, 277, 749-760.	2.2	147
121	Engineering synergy in biotechnology. Nature Chemical Biology, 2014, 10, 319-322.	3.9	147
122	Personal model-assisted identification of NAD ⁺ and Glutathione metabolism as intervention target in NAFLD. Molecular Systems Biology, 2017, 13, 916.	3.2	147
123	Fatty acid synthesis is required for breast cancer brain metastasis. Nature Cancer, 2021, 2, 414-428.	5.7	147
124	Barriers and opportunities in bio-based production of hydrocarbons. Nature Energy, 2018, 3, 925-935.	19.8	146
125	The role of biofuels in the future energy supply. Energy and Environmental Science, 2013, 6, 1077.	15.6	145
126	Industrial Systems Biology of <i>Saccharomyces cerevisiae</i> Enables Novel Succinic Acid Cell Factory. PLoS ONE, 2013, 8, e54144.	1.1	142

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127	The genome-scale metabolic model iIN800 of <i>Saccharomyces cerevisiae</i> and its validation: a scaffold to query lipid metabolism. <i>BMC Systems Biology</i> , 2008, 2, 71.	3.0	141
128	Regulation of amino-acid metabolism controls flux to lipid accumulation in <i>Yarrowia lipolytica</i> . <i>Npj Systems Biology and Applications</i> , 2016, 2, 16005.	1.4	141
129	DCEO Biotechnology: Tools To Design, Construct, Evaluate, and Optimize the Metabolic Pathway for Biosynthesis of Chemicals. <i>Chemical Reviews</i> , 2018, 118, 4-72.	23.0	141
130	Anaerobic and aerobic batch cultivations of <i>Saccharomyces cerevisiae</i> mutants impaired in glycerol synthesis. <i>Yeast</i> , 2000, 16, 463-474.	0.8	140
131	Microfluidic screening and whole-genome sequencing identifies mutations associated with improved protein secretion by yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E4689-96.	3.3	138
132	Metabolic cooperation and spatiotemporal niche partitioning in a kefir microbial community. <i>Nature Microbiology</i> , 2021, 6, 196-208.	5.9	138
133	Unravelling evolutionary strategies of yeast for improving galactose utilization through integrated systems level analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12179-12184.	3.3	137
134	Succinate dehydrogenase inhibition leads to epithelial-mesenchymal transition and reprogrammed carbon metabolism. <i>Cancer & Metabolism</i> , 2014, 2, 21.	2.4	137
135	Combining mechanistic and machine learning models for predictive engineering and optimization of tryptophan metabolism. <i>Nature Communications</i> , 2020, 11, 4880.	5.8	137
136	Large-Scale Evaluation of In Silico Gene Deletions in <i>Saccharomyces cerevisiae</i> . <i>OMICS A Journal of Integrative Biology</i> , 2003, 7, 193-202.	1.0	135
137	A Closer Look at <i>Bacteroides</i> : Phylogenetic Relationship and Genomic Implications of a Life in the Human Gut. <i>Microbial Ecology</i> , 2011, 61, 473-485.	1.4	135
138	Morphology and physiology of an α -amylase producing strain of <i>Aspergillus oryzae</i> during batch cultivations. <i>Biotechnology and Bioengineering</i> , 2000, 49, 266-276.	1.7	134
139	Post-genomic insights into the plant polysaccharide degradation potential of <i>Aspergillus nidulans</i> and comparison to <i>Aspergillus niger</i> and <i>Aspergillus oryzae</i> . <i>Fungal Genetics and Biology</i> , 2009, 46, S161-S169.	0.9	133
140	Systems medicine and metabolic modelling. <i>Journal of Internal Medicine</i> , 2012, 271, 142-154.	2.7	133
141	Integrated Network Analysis Reveals an Association between Plasma Mannose Levels and Insulin Resistance. <i>Cell Metabolism</i> , 2016, 24, 172-184.	7.2	133
142	Systems Biology of Metabolism: A Driver for Developing Personalized and Precision Medicine. <i>Cell Metabolism</i> , 2017, 25, 572-579.	7.2	132
143	Bioreaction Engineering Principles. , 2003, , .		132
144	On-line and in situ monitoring of biomass in submerged cultivations. <i>Trends in Biotechnology</i> , 1997, 15, 517-522.	4.9	131

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145	Integration of metabolome data with metabolic networks reveals reporter reactions. <i>Molecular Systems Biology</i> , 2006, 2, 50.	3.2	131
146	Impact of systems biology on metabolic engineering of <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2008, 8, 122-131.	1.1	131
147	Antibiotic Overproduction in <i>Streptomyces coelicolor</i> A3(2) Mediated by Phosphofructokinase Deletion*. <i>Journal of Biological Chemistry</i> , 2008, 283, 25186-25199.	1.6	131
148	Flux Control at the Malonyl-CoA Node through Hierarchical Dynamic Pathway Regulation in <i>Saccharomyces cerevisiae</i> . <i>ACS Synthetic Biology</i> , 2016, 5, 224-233.	1.9	131
149	Metabolic engineering: Techniques for analysis of targets for genetic manipulations. , 1998, 58, 125-132.		130
150	Industrial systems biology. <i>Biotechnology and Bioengineering</i> , 2010, 105, 439-460.	1.7	130
151	Molecular Basis for Mycophenolic Acid Biosynthesis in <i>Penicillium brevicompactum</i> . <i>Applied and Environmental Microbiology</i> , 2011, 77, 3035-3043.	1.4	130
152	Combined metabolic engineering of precursor and co-factor supply to increase Î±-santalene production by <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2012, 11, 117.	1.9	130
153	Transcriptomics resources of human tissues andÂorgans. <i>Molecular Systems Biology</i> , 2016, 12, 862.	3.2	130
154	Biobased organic acids production by metabolically engineered microorganisms. <i>Current Opinion in Biotechnology</i> , 2016, 37, 165-172.	3.3	130
155	Metabolic engineering of yeast for fermentative production of flavonoids. <i>Bioresource Technology</i> , 2017, 245, 1645-1654.	4.8	129
156	Synergies between synthetic biology and metabolic engineering. <i>Nature Biotechnology</i> , 2011, 29, 693-695.	9.4	128
157	Different expression systems for production of recombinant proteins in <i>Saccharomyces cerevisiae</i> . <i>Biotechnology and Bioengineering</i> , 2012, 109, 1259-1268.	1.7	128
158	Chromosome 3p loss of heterozygosity is associated with a unique metabolic network in clear cell renal carcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E866-75.	3.3	128
159	Enhancement of farnesyl diphosphate pool as direct precursor of sesquiterpenes through metabolic engineering of the mevalonate pathway in <i>Saccharomyces cerevisiae</i> . <i>Biotechnology and Bioengineering</i> , 2010, 106, 86-96.	1.7	127
160	Coupled incremental precursor and co-factor supply improves 3-hydroxypropionic acid production in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2014, 22, 104-109.	3.6	123
161	Metabolic footprinting in microbiology: methods and applications in functional genomics and biotechnology. <i>Trends in Biotechnology</i> , 2008, 26, 490-497.	4.9	122
162	Engineering yeast for high-level production of stilbenoid antioxidants. <i>Scientific Reports</i> , 2016, 6, 36827.	1.6	122

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163	Imidazole propionate is increased in diabetes and associated with dietary patterns and altered microbial ecology. <i>Nature Communications</i> , 2020, 11, 5881.	5.8	122
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